

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2002, 10:08:05 ; Search time 1866.06 Seconds
(without alignments)
5607.145 Million cell updates/sec

Title: US-09-743-194-4

Perfect score: 500
Sequence: 1 ggaagtcctgcctacagcg.....tacggttatacataatcat 500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapect 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_com:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_to:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID Description
SUMMARIES

1	497	99.4	1400	8	SCYOLL10W	Z74852 S. cerevisia
2	497	99.4	44019	8	SCCHRXY44	Z48149 S. cerevisia
3	497	80.8	1541	8	SCYOLL10W	Z74851 S. cerevisia
4	160	32.0	848	11	CNS0618W	AL399990 T7 end of
5	141	28.2	1671	8	SCUI18313	U18313 Saccharomyc
6	73.4	14.7	7218	6	166494	166494 Sequence 14
7	66.2	13.2	156550	2	AC015830	AC015830 Homo sapi
8	65.2	13.0	143585	2	AC013349	AC013349 Homo sapi
9	65	13.0	52359	2	AC010772	AC010772 Homo sapi
10	64	12.8	64789	2	AC083839	AC083839 Homo sapi
11	63.6	12.7	887	11	CNS06K84	AL403274 T7 end of
12	63.6	12.7	6868	6	AX346599	AX346599 Sequence
13	63.6	12.7	196502	2	AL359957	AL359957 Homo sapi
14	63.4	12.7	83440	2	AC024285	AC024285 Homo sapi
15	63	12.6	8087	2	AC106848	AC106848 Homo sapi
16	63	12.6	70511	2	AC091083	AC091083 Homo sapi
17	62.8	12.6	81120	2	AC022851	AC022851 Homo sapi
18	62.2	12.4	56693	2	AC084077	AC084077 Homo sapi
19	62	12.4	7058	6	AX348438	AX348438 Sequence
20	62	12.4	14006	6	AX346860	AX346860 Sequence
21	62	12.4	72386	2	AC102703	AC102703 Mus muscu
22	62	12.4	179902	2	AP003630	AP003630 Oryza sat
23	62	12.4	231972	2	AC068055	AC068055 Homo sapi
24	61.8	12.4	45685	2	HS3337540	AL3337540 Homo sapi
25	61.8	12.4	45685	2	AC087168	AC087168 Homo sapi
26	61.8	12.4	63365	2	AC087437	AC087437 Homo sapi
27	61.6	12.3	56857	2	AC021917	AC021917 Homo sapi
28	61.6	12.3	6070	6	AX281468	AX281468 Sequence
29	61.2	12.2	6070	6	AX346581	AX346581 Sequence
30	61.2	12.2	6070	6	AX348804	AX348804 Sequence
31	61.2	12.2	131271	2	AC015927	AC015927 Homo sapi
32	61.2	12.2	131271	2	AC015927	AC015927 Homo sapi
33	60.8	12.2	78227	2	AC067768	AC067768 Homo sapi
34	60.6	12.1	349980	6	AX344566	AX344566 Sequence
35	60.4	12.1	6668	6	AX346598	AX346598 Sequence
36	60.4	12.1	99263	2	CNS01DX9	AL139177 Homo sapi
37	60.4	12.1	125876	2	AC026380	AC026380 Mus muscu
38	60.4	12.1	181413	2	AC023818	AC023818 Homo sapi
39	60.2	12.0	64767	2	AC102701	AC102701 Mus muscu
40	60.2	12.0	66240	2	AC090633	AC090633 Homo sapi
41	60.2	12.0	71751	2	AC090222	AC090222 Homo sapi
42	60.2	12.0	74119	2	AC036177	AC036177 Homo sapi
43	60	12.0	60565	2	AC023852	AC023852 Homo sapi
44	59.6	11.9	9539	6	AX277889	AX277889 Sequence
45	59.6	11.9	9539	6	AX323566	AX323566 Sequence

ALIGNMENTS

RESULT 1
LOCUS SCYOLL10W 1400 bp DNA linear PLN 11-AUG-1997
DEFINITION S.cerevisiae chromosome XV reading frame ORF YOLL10W.
ACCESSION Z74852 Y13140
VERSION Z74852.1 GI:1419976
KEYWORDS
SOURCE
ORGANISM
baker's yeast.
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE
1 (bases 1 to 1400)
AUTHORS Durand,P., Hilger,F., Portetelle,D. and Vandenbol,M.
JOURNAL Unpublished
REFERENCE
MIPS 2 (bases 1 to 1400)
JOURNAL Direct Submission
Submitted (04-JUL-1996) Data collected by MIPS on behalf of the
European yeast chromosome XV sequencing project. MIPS at the
Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152
Martinsried, FRG; E-mail: Mewes@mips.embl.net.org
FEATURES
source
1. 1400

/organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"
/chromosome="XV"
280..993
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GWRNLSGLLMDLGLGMSWVLPGLLSRPVFOBSALDEQYVALQNSPGILLHENGVAL
VLPSSGCSLDPEVVPK"

BASE COUNT 303 a 303 c 332 g 462 t
ORIGIN

Query Match 99.4% Score 497; DB 8; Length 1400;
Best Local Similarity 100.0%; Pred. No. 2.5e-111;
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggaagtcgtctcagagcgaggtgctgagctatgccccagcgctccgagctccta 60
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Db 901 ggagctgctctcagagcgaggtgctgagctatgccccagcgctccgagctccta 60
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QY 61 tccctagattcgtgctgccccagagctaaagctgagctttagagtgagcaca 120
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QY 121 gggctttagctgctttagatcagagcgagctttagctcagagctttagatc 180
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Db 1021 gggctttagctgctttagatcagagcgagctttagctcagagctttagatc 180
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QY 181 aattaagcttcttaccatatttattatcatctttagtaagctgagctcctg 240
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Db 1081 aattaagcttcttaccatatttattatcatctttagtaagctgagctcctg 240
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QY 241 tctctgctgcttctgctgagcttctctctctctctgcttctgctgctcctc 300
|||
Db 1141 tctctgctgcttctgctgagcttctctctctctctgcttctgctgctcctc 300
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QY 301 ccgaatgagctatagcgatataatagagcgagctttagcagagatcatctcag 360
|||
Db 1201 ccgaatgagctatagcgatataatagagcgagctttagcagagatcatctcag 360
|||
QY 361 tctctgagcttcttcttcttcttcttcttcttcttcttcttcttcttctt 420
|||
Db 1261 tctctgagcttcttcttcttcttcttcttcttcttcttcttcttcttctt 420
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QY 421 tctttagctgcttcttcttcttcttcttcttcttcttcttcttcttctt 480
|||
Db 1321 tctttagctgcttcttcttcttcttcttcttcttcttcttcttcttctt 480
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QY 481 taagttataatcaatca 497
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Db 1381 taagttataatcaatca 497
|||

RESULT 2
SCCHRXYV4 44019 bp DNA linear JUN 24-MAR-1997
LOCUS S.cerevisiae chromosome XV DNA (44 kb fragment).
DEFINITION 248149.1 GI:663234
ACCESSION 248149.1 GI:663234
KEYWORDS retrotransposon; su1(+); frameshift suppressor; tRNA-Gly; tRNA-Thr;
tyl-H3.
SOURCE baker's yeast.
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

REFERENCE
AUTHORS Vandebol,M., Durand,P., Portetalle,D. and Hilger,F.
TITLE Sequence analysis of a 44 Kb DNA fragment of yeast chromosome XV
including the tyl-H3 retrotransposon, the su1(+), frameshift
suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr1a and a
delta element
JOURNAL Yeast 11 (11), 1069-1075 (1995)
MEDLINE 96076631
REFERENCE 2 (bases 1 to 44019)
AUTHORS John,T.R., Ghosh,M. and Johnson,J.D.
TITLE Identification and expression of the Saccharomyces cerevisiae
cytoplasmic tyriophanyl-tRNA synthetase gene
JOURNAL Yeast 13 (1), 37-41 (1997)
MEDLINE 97197969
REFERENCE 3 (bases 1 to 44019)
AUTHORS Hilger,F.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1995) Hilger F., Faculte des Sciences
Agronomiques de Gembloux, UER de Microbiologie, Avenue Marechal
Julin, 6, 5030 Gembloux, Belgium
Location/Qualifiers
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/db_xref="taxon:4932"
627..4033
/gene="orf"
627..2564
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DQIDGNTFELISDFEVLAPKWEVFLDIEVDENKICKIDFQNFNDQSPWILR
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NOLSEVSNLQYIILEYNTARINNRELEKKEIDFPEMISKSLFSGQSLVLIYT
SKVIFLSDSENDSPALMKRYDRKELEKMEVLYLKHLEMKLEKREKITSLEFKF
ILSGELFTSMILEAISDKINPFGDQVIAIGSIVLVLDVYRCFAQJELQMLNS
ILILPELSEVSLIGIIDIYLAQTLKMKIRIALVCSISIDILSMQISDDMBND
DLITLIMSEIKMNSVYFKLDTSDLYVEGDENKVMPLRCSKEEFRLMISDDEET
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LYISSNSQSRQSPNLOKVPNHNENAVESNAQESVPTPEEORYETKGLRKRIYCTR
PEFLKSPHVEVMEVKEYTEGVNGQPSIRKMEALYQTMARDPANNKRYRRRYLWKA
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/translation="WGAKSVYASSSKRIKRNNGKVKYKSKRIKVRKPKQGISLNDEN
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Oy 361 ttctgtatagacccttctacttacttacttctgttttaaccctacttacttactt 420
Db 13233 TTTGCTTGATAGACCTTTACTTACTTACTTCTGTTTAACTTCATTTACTTACTT 13292
Oy 421 tcttgatcggttttttctctgctatctaaagtcaaaatcaaaagaaacatagaaac 480
Db 13293 TCTTGATCGGTTTCTTCTGCTGTAAGTCAAACTCAATCAACAAACATCAAAAC 13352
Oy 481 taagttatatacaatca 497
Db 13353 TAGCTTTATATCAATTA 13369

RESULT 3
SCYOL109W 1541 bp DNA linear PLN 05-AUG-1997
LOCUS S.cerevisiae chromosome XV reading frame ORF YOL109W.
DEFINITION 274851.Y13140
ACCESSION 274851.1 GI:1419974
VERSION 274851.1 GI:1419974
KEYWORDS
SOURCE Baker's yeast.
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 1541)
AUTHORS Durand,P., Hilger,F., Portetelle,D. and Vandenbol,M.
JOURNAL Unpublished
TITLE 2 (bases 1 to 1541)
MIPS.
REFERENCE Direct Submission
TITLE Submitted (04-JUL-1996) Data collected by MIPS on behalf of the
AUTHORS European yeast chromosome XV sequencing project. MIPS at the
JOURNAL Mex-Planck-Institut fuer Biochemie, Am Klopfersplitz 18a D-82152
Martinsried, FRG. E-mail: Mewes@mips.emblnet.org

FEATURES
Source
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location/Qualifiers
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KINRRTASIFN"
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BASE COUNT 525 a 266 c 273 g 477 t
ORIGIN
Query Match 80.8%; Score 404; DB 8; Length 1541;
Best Local Similarity 100.0%; Pred. No. 1,4e-88;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 94 ttaaacgtggtttatggtgacacaggtttatcggtttatcgaagcgatt 153
Db 1 TTTAAACGTGTGTTATGGTGACACAGGCTTTATCGTGTATATGATGCGCATTT 60
Oy 154 gtgctcagtgattttatgatatcaatcaagttctactaatatttattac 213
Db 61 GTGCTCAGTGATTTTGTATATCCATTAAGTTTCTACTAATTTATTTATAC 120
Oy 214 atctttagttaaagcggttctgctctgttctgctcttctgfgcggtctctct 273

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Db 121 ANCTTAGTATAGCTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 160
Oy 274 cttgttctcgtgtgtgtcccccacgcgcagtgactatargcgtatataatagac 333
Db 181 CTGTGTTCTGCTGTGTGTCGCCCATCGCCGATGGCTTATATAGCGATATAGAC 240
Oy 334 gatttttagtgcgaatcatctcagtttgcgttagccttctacttatttcttc 393
Db 241 GATTTTATAGCTGAGATGATCATCTGATTCATACCTTTCTACTTATTTACTTC 300
Oy 394 gttttaaactaatatacttagtttctcttgcgcgtttcttctctgatactaa 453
Db 301 GTTTTAACTCATATATATCTTATGTTTCTTTCATGCTGTTTCTGCTGATCTTAA 360
Oy 454 agttcaatcaagaacatacaaaactacgtttatataatca 497
Db 361 AGTTCAAAATCAAGAAACATCAAACTACGTTATATCAATTA 404

RESULT 4
CNS0618W 848 bp DNA linear STS 10-JAN-2001
LOCUS T7 end of clone AS0A018601 of library AS0A from strain CLIB 533
DEFINITION
ACCESSION ALJ99990
VERSION ALJ99990.1 GI:12155259
KEYWORDS STS.
SOURCE Saccharomyces bayanus.
ORGANISM Saccharomyces bayanus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 848)
AUTHORS Bon,E., Neuveglise,C., Casaregola,S., Artiguenave,F., Wincker,P.,
Aigle,M. and Durrens,P.
JOURNAL Genomic Exploration of the Hemiascomycetous Yeasts: 5.
TITLE Saccharomyces bayanus var. uvarum
PUBMED FEBS Lett. 487 (1), 37-41 (2000)
11152860
2 (bases 1 to 848)
Soudier,U.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Leplinge,A., Llorente,B.,
Maupertuy,A., Neuveglise,C., Olier-Kalogeropoulos,O., Potter,S.,
Saurin,M., Tekala,F., Toffano-Nicche,C., Wesolowski-Louvel,M.,
Wincker,P. and Walsenbach,J.
JOURNAL Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of
PUBMED yeast species for molecular evolution studies(1)
11152876
3 (bases 1 to 848)
Genoscope.
REFERENCE Direct Submission
AUTHORS Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
TITLE 2 rue Gaston Cremlieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
JOURNAL sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This STS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
anansua, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
location/Qualifiers
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/variety="uvarum"
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1	ggaagtcctcctccagacgacgctgtgcgcctagctatctgcccgacgctccggtgctcta	60		
94	gscgcagactgctccacagacgcggtgtgagccttacctgcccacgacgctccgggtgctcta	153		
QY	61 tcccaagatttcgtgcgtcccccagcccaacagctaaacgtgtgtgttlaacggtgaccca	120		
Db	154 tccctggattttgtcgtcccccagccacacacacgaatgctgtgtgtgtgtgtgtgtgt	213		
QY	121 gggcttaccgtgtttatcatcgatgacgatttgcctccagtgatattttgatatcc	180		
Db	214 agcgttttaccggtttatcatcatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	271		
QY	181 aattaggttttcccaatttattttatcaacttaagcttaagcttgaatgctgtgtctg	240		
Db	272 -----ttttctttacttaatttttttttttttttttttttttttttttttttttt	321		
QY	241 ttctcgtcgtcttcgtgcggttcctctctctctctctctctctctctctctctctct	300		
Db	322 gttctctgtattttctctgtgcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	381		
QY	301 ccgatggcttatatgcgcataatataatagacgaatttttaacgtcgaagatcatctcag	360		
Db	382 ccccatcgctt--caatgcgtatattattatfarracgcggttttcaggtcgaaagatcatctata	439		
QY	361 ttctgtctgatatgccttctacttatttacttctcgtttt	398		
Db	440 ctttctgtgattaaccttttctcttcttacttcttcttctt	477		

BASE COUNT	369 a	359 c	442 g	501 t
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Query Match	28.2%	Score 141;	DB 8;	Length 1671;
Best Local Similarity	100.0%	Pred. No. 2,8e-24;		
Matches 141;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ggaggtctgcttacgacgacggtgctgagctatgtccgcgaaggtctcggtgtgcta 60		
DB	1531	GGAGGTCTGCTTCAACAGACGGCGTGTCGCTAGATTGCCCCGACGGGTCCGGGTGCTTA 1590		
QY	61	tcctagattctgctggtcccgaccacaatagtaaacgtgtgtttagtggtgacaca 120		
DB	1591	TCCCTNAGATTTCGTGTGTGTCGCCGACCCCAATAGTTAAACGTGTGTTATGTGTACACA 1650		
QY	121	ggagcttaccgtgtttatat 141		
DB	1651	GGGCTTATCTGCTTTATAT 1671		
RESULT	6			
166494	166494	7218 bp	DNA	linear
LOCUS				PAT 28-DEC-1997
DEFINITION	Sequence 14 from patent US 5670367.			
ACCESSION	166494			
VERSION	166494.1	GI:2724471		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 7218)			
AUTHORS	Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.			
TITLE	Recombinant fowlpox virus			
JOURNAL	Patent: US 5670367-A 14-23-SEP-1997;			
FEATURES	Location/Qualifiers			
source	1..7218			
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ORIGIN				368 others
Query Match	14.7%	Score 73.4;	DB 6;	Length 7218;
Best Local Similarity	7.6%	Pred. No. 1.1e-07;		
Matches 29;	Conservative 219;	Mismatches 139;	Indels 0;	Gaps 0
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DB	1003	TTCGTTGCCATACGCTCACGAAATTATCCGAGCTTGCTGCAGCTCGAGGAGCTTG 1062		
QY	130	cgtgttataatcgaatgacgatctgtgctccacagtcatttttgcataccaataagtc 189		
DB	1063	CGAT 1122		
QY	190	ttcttaactaatattattattacatccttagttaatgctgtgtgtcgtctgtctgctg 249		

33473	36404:	contlg of 932 bp	in length
35405	36504:	gap of 100 bp	
36505	3734:	contlg of 930 bp	in length
37435	37534:	gap of 100 bp	
37535	38447:	contlg of 913 bp	in length
38448	38547:	gap of 100 bp	
38548	39476:	contlg of 929 bp	in length
39477	39576:	gap of 100 bp	
39577	40517:	contlg of 941 bp	in length
40518	41526:	contlg of 909 bp	in length
41527	41626:	gap of 100 bp	
41627	42519:	contlg of 893 bp	in length
42520	42619:	gap of 100 bp	
42620	43495:	contlg of 876 bp	in length
43496	43595:	gap of 100 bp	
43596	44503:	contlg of 908 bp	in length
44504	44603:	gap of 100 bp	
44604	45488:	contlg of 885 bp	in length
45489	45588:	gap of 100 bp	
45589	46500:	contlg of 932 bp	in length
46521	46620:	gap of 100 bp	
46621	47537:	contlg of 917 bp	in length
47538	47637:	gap of 100 bp	
47638	48575:	contlg of 938 bp	in length
48576	48675:	gap of 100 bp	
48676	49600:	contlg of 925 bp	in length
49601	49700:	gap of 100 bp	
49701	50588:	contlg of 888 bp	in length
50589	50688:	gap of 100 bp	
50689	51624:	contlg of 936 bp	in length
51625	51724:	gap of 100 bp	
51725	52607:	contlg of 883 bp	in length
52608	52707:	gap of 100 bp	
52708	53630:	contlg of 923 bp	in length
53631	53730:	gap of 100 bp	
53731	54664:	contlg of 914 bp	in length
54665	54744:	gap of 100 bp	
54745	55704:	contlg of 960 bp	in length
55705	55804:	gap of 100 bp	
55805	56722:	contlg of 918 bp	in length
56723	56822:	gap of 100 bp	
56823	57739:	contlg of 917 bp	in length
57740	57839:	gap of 100 bp	
57840	58766:	contlg of 927 bp	in length
58767	58866:	gap of 100 bp	
58867	59775:	contlg of 909 bp	in length
59776	59875:	gap of 100 bp	
59876	60784:	contlg of 909 bp	in length
60785	60884:	gap of 100 bp	
60885	61795:	contlg of 911 bp	in length
61796	61895:	gap of 100 bp	
61896	62811:	contlg of 922 bp	in length
62818	62917:	gap of 100 bp	
62918	63841:	contlg of 924 bp	in length
63842	63941:	gap of 100 bp	
63942	64851:	contlg of 910 bp	in length
64852	64951:	gap of 100 bp	
64952	65844:	contlg of 897 bp	in length
65845	65948:	gap of 100 bp	
65949	66855:	contlg of 911 bp	in length
66860	66959:	gap of 100 bp	
66960	67875:	contlg of 916 bp	in length
67876	67975:	gap of 100 bp	
67977	68879:	contlg of 904 bp	in length
68880	68979:	gap of 100 bp	
68980	69907:	contlg of 928 bp	in length
69908	70007:	gap of 100 bp	
70008	70861:	contlg of 854 bp	in length
70862	70961:	gap of 100 bp	
70962	71880:	contlg of 919 bp	in length
71881	71980:	gap of 100 bp	
71981	72915:	contlg of 935 bp	in length

[illegible]

	RESULT	8
AC013349	AC013349	143585 bp DNA linear HTG 13-JUL-2001
LOCUS	Homo sapiens clone RP11-22K1, LOW-PASS SEQUENCE SAMPLING.	
DEFINITION	AC013349	
ACCSSION	AC013349.3 GI:9124043	
VERSION	HTG: HTGS_PHASE0.	
KEYWORDS	human.	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 143585)	
REFERENCE	Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-22K1 Unpublished 2 (bases 1 to 143585) Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barua,N., Beckely,R., Boguslavsky,L., Boukhalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collamore,A., Cooke,P., Dearlano,W., Dewar,K., Domono,M., Donelan,L., Doyle,M., Ferreira,P., Fitzhugh,K., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hages,B., Heathford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lewczak,J.C., Lien,C., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,P., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,J., Peterson,K., Pollara,V., Riley.R., Roy.A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.	
TITLE	JOURNAL	
JOURNAL	Submitted (06-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced g1:6910730. All repeats were identified using RepeatMasker: Smith, A.F & Green, P. (1996-1997) http://ftp.genome.washington.edu/RW/RepeatMasker.html -----Genome Center	
COMMENT		

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: <http://www.seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center Project name: L4134
Center Clone name: 22_K_1

* NOTE: This record contains 150 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be generic-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 930: contig of 930 bp in length
* 931 1030: gap of 100 bp
* 1031 1955: contig of 925 bp in length
* 1956 2055: gap of 100 bp
* 2056 2959: contig of 904 bp in length
* 2960 3059: gap of 100 bp
* 3060 4006: contig of 947 bp in length
* 4007 4106: gap of 100 bp
* 4107 4966: contig of 860 bp in length
* 4967 5066: gap of 100 bp
* 5067 5944: contig of 878 bp in length
* 5945 6044: gap of 100 bp
* 6045 6906: contig of 862 bp in length
* 6907 7006: gap of 100 bp
* 7007 7851: contig of 845 bp in length
* 7852 7951: gap of 100 bp
* 7952 8788: contig of 837 bp in length
* 8789 8888: gap of 100 bp
* 8889 9781: contig of 893 bp in length
* 9782 9881: gap of 100 bp
* 9882 10795: contig of 914 bp in length
* 10796 10895: gap of 100 bp
* 10896 11769: contig of 874 bp in length
* 11770 11869: gap of 100 bp
* 11870 12764: contig of 895 bp in length
* 12765 12864: gap of 100 bp
* 12865 13757: contig of 893 bp in length
* 13758 13857: gap of 100 bp
* 13858 14755: contig of 898 bp in length
* 14756 14855: gap of 100 bp
* 14856 15765: contig of 910 bp in length
* 15766 15865: gap of 100 bp
* 15866 16759: contig of 894 bp in length
* 16760 16859: gap of 100 bp
* 16860 17730: contig of 871 bp in length
* 17731 17830: gap of 100 bp
* 17831 18747: contig of 917 bp in length
* 18748 18847: gap of 100 bp
* 18848 19779: contig of 932 bp in length
* 19780 19879: gap of 100 bp
* 19880 20741: contig of 862 bp in length
* 20742 20841: gap of 100 bp
* 20842 21701: contig of 860 bp in length
* 21702 21801: gap of 100 bp
* 21802 22665: contig of 864 bp in length
* 22666 22765: gap of 100 bp
* 22766 23630: contig of 865 bp in length
* 23631 23730: gap of 100 bp
* 23731 24622: contig of 892 bp in length
* 24623 24722: gap of 100 bp
* 24723 25634: contig of 912 bp in length
* 25635 25734: gap of 100 bp
* 25735 26609: contig of 875 bp in length
* 26610 26709: gap of 100 bp
* 26710 27615: contig of 906 bp in length
* 27616 27715: gap of 100 bp
* 27716 28571: contig of 856 bp in length

* 28572 28671: gap of 100 bp
* 28672 29562: contig of 891 bp in length
* 29563 29662: gap of 100 bp
* 29663 30566: contig of 904 bp in length
* 30567 30666: gap of 100 bp
* 30667 31587: contig of 921 bp in length
* 31588 31687: gap of 100 bp
* 31688 32572: contig of 885 bp in length
* 32573 32672: gap of 100 bp
* 32673 33572: contig of 900 bp in length
* 33573 33672: gap of 100 bp
* 33673 34536: contig of 864 bp in length
* 34537 34636: gap of 100 bp
* 34637 35545: contig of 909 bp in length
* 35546 35645: gap of 100 bp
* 35646 36496: contig of 851 bp in length
* 36497 36596: gap of 100 bp
* 36597 37492: contig of 896 bp in length
* 37493 37592: gap of 100 bp
* 37593 38504: contig of 912 bp in length
* 38505 38604: gap of 100 bp
* 38605 39523: contig of 919 bp in length
* 39524 39623: gap of 100 bp
* 39624 40469: contig of 846 bp in length
* 40470 40569: gap of 100 bp
* 40570 41446: contig of 877 bp in length
* 41447 41546: gap of 100 bp
* 41547 42418: contig of 872 bp in length
* 42419 42518: gap of 100 bp
* 42519 43377: contig of 859 bp in length
* 43378 43477: gap of 100 bp
* 43478 44333: contig of 856 bp in length
* 44334 44433: gap of 100 bp
* 44434 45324: contig of 891 bp in length
* 45325 45424: gap of 100 bp
* 45425 46337: contig of 913 bp in length
* 46338 46437: gap of 100 bp
* 46438 47340: contig of 903 bp in length
* 47341 47440: gap of 100 bp
* 47441 48330: contig of 890 bp in length
* 48331 48430: gap of 100 bp
* 48431 49328: contig of 898 bp in length
* 49329 49428: gap of 100 bp
* 49429 50312: contig of 884 bp in length
* 50313 50412: gap of 100 bp
* 50413 51292: contig of 880 bp in length
* 51293 51392: gap of 100 bp
* 51393 52229: contig of 837 bp in length
* 52230 52329: gap of 100 bp
* 52330 53186: contig of 857 bp in length
* 53187 53286: gap of 100 bp
* 53287 54219: contig of 933 bp in length
* 54220 54319: gap of 100 bp
* 54320 55206: contig of 887 bp in length
* 55207 55306: gap of 100 bp
* 55307 56208: contig of 902 bp in length
* 56209 56308: gap of 100 bp
* 56309 57218: contig of 910 bp in length
* 57219 57318: gap of 100 bp
* 57319 58231: contig of 913 bp in length
* 58232 58331: gap of 100 bp
* 58332 59246: contig of 915 bp in length
* 59247 59346: gap of 100 bp
* 59347 60241: contig of 895 bp in length
* 60242 60341: gap of 100 bp
* 60342 61250: contig of 909 bp in length
* 61251 61350: gap of 100 bp
* 61351 62216: contig of 866 bp in length
* 62217 62316: gap of 100 bp
* 62317 63190: contig of 874 bp in length
* 63191 63290: gap of 100 bp
* 63291 64198: contig of 906 bp in length
* 64199 64298: gap of 100 bp

Center code: MIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

Project Information
Center project name: L11300
Center clone name: j179_L_5

* NOTE: This record contains 81 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 736: contig of 736 bp in length
* 737 836: gap of 100 bp
* 837 1529: contig of 693 bp in length
* 1530 1629: gap of 100 bp
* 1630 2344: contig of 715 bp in length
* 2345 2444: gap of 100 bp
* 2445 3153: contig of 709 bp in length
* 3154 3253: gap of 100 bp
* 3254 3946: contig of 693 bp in length
* 3947 4046: gap of 100 bp
* 4047 4749: contig of 703 bp in length
* 4750 4849: gap of 100 bp
* 4850 5562: contig of 713 bp in length
* 5563 5662: gap of 100 bp
* 5663 6355: contig of 693 bp in length
* 6356 6455: gap of 100 bp
* 6456 7163: contig of 708 bp in length
* 7164 7263: gap of 100 bp
* 7264 7939: contig of 676 bp in length
* 7940 8039: gap of 100 bp
* 8040 8747: contig of 708 bp in length
* 8748 8847: gap of 100 bp
* 8848 9570: contig of 723 bp in length
* 9571 9670: gap of 100 bp
* 9671 10390: contig of 720 bp in length
* 10391 10490: gap of 100 bp
* 10491 11192: contig of 702 bp in length
* 11193 11292: gap of 100 bp
* 11293 11989: contig of 697 bp in length
* 11990 12089: gap of 100 bp
* 12090 12781: contig of 692 bp in length
* 12782 12881: gap of 100 bp
* 12882 13583: contig of 702 bp in length
* 13584 13683: gap of 100 bp
* 13684 14387: contig of 704 bp in length
* 14388 14487: gap of 100 bp
* 14488 15187: contig of 700 bp in length
* 15188 15287: gap of 100 bp
* 15288 16002: contig of 715 bp in length
* 16003 16102: gap of 100 bp
* 16103 16822: contig of 720 bp in length
* 16823 16922: gap of 100 bp
* 16923 17651: contig of 729 bp in length
* 17652 17751: gap of 100 bp
* 17752 18402: contig of 651 bp in length
* 18403 18502: gap of 100 bp
* 18503 19210: contig of 708 bp in length
* 19211 19310: gap of 100 bp
* 19311 20005: contig of 695 bp in length
* 20006 20105: gap of 100 bp
* 20106 20791: contig of 686 bp in length
* 20792 20891: gap of 100 bp
* 20892 21595: contig of 704 bp in length
* 21596 21695: gap of 100 bp
* 21696 22391: contig of 696 bp in length

* 22392 22491: gap of 100 bp
* 22492 23181: contig of 690 bp in length
* 23182 23281: gap of 100 bp
* 23282 23984: contig of 703 bp in length
* 23985 24084: gap of 100 bp
* 24085 24804: contig of 720 bp in length
* 24805 24904: gap of 100 bp
* 24905 25609: contig of 705 bp in length
* 25610 25709: gap of 100 bp
* 25710 26406: contig of 697 bp in length
* 26407 26505: gap of 100 bp
* 26507 27207: contig of 701 bp in length
* 27208 27307: gap of 100 bp
* 27308 28009: contig of 702 bp in length
* 28010 28109: gap of 100 bp
* 28110 28793: contig of 684 bp in length
* 28794 28893: gap of 100 bp
* 28894 29580: contig of 687 bp in length
* 29581 29680: gap of 100 bp
* 29681 30390: contig of 710 bp in length
* 30391 30490: gap of 100 bp
* 30491 31180: contig of 690 bp in length
* 31181 31280: gap of 100 bp
* 31281 31988: contig of 708 bp in length
* 31989 32088: gap of 100 bp
* 32089 32803: contig of 715 bp in length
* 32804 32903: gap of 100 bp
* 32904 33631: contig of 728 bp in length
* 33632 33731: gap of 100 bp
* 33732 34404: contig of 673 bp in length
* 34405 34504: gap of 100 bp
* 34505 35201: contig of 697 bp in length
* 35202 35301: gap of 100 bp
* 35302 36002: contig of 701 bp in length
* 36003 36102: gap of 100 bp
* 36103 36782: contig of 680 bp in length
* 36783 36882: gap of 100 bp
* 36883 37574: contig of 692 bp in length
* 37575 37674: gap of 100 bp
* 37675 38360: contig of 666 bp in length
* 38361 38460: gap of 100 bp
* 38461 39145: contig of 685 bp in length
* 39146 39245: gap of 100 bp
* 39246 39948: contig of 703 bp in length
* 39949 40048: gap of 100 bp
* 40049 40772: contig of 724 bp in length
* 40773 40872: gap of 100 bp
* 40873 41580: contig of 708 bp in length
* 41581 41680: gap of 100 bp
* 41681 42364: contig of 684 bp in length
* 42365 42464: gap of 100 bp
* 42465 43162: contig of 698 bp in length
* 43163 43262: gap of 100 bp
* 43263 43945: contig of 683 bp in length
* 43946 44045: gap of 100 bp
* 44046 44749: contig of 704 bp in length
* 44750 44849: gap of 100 bp
* 44850 45551: contig of 702 bp in length
* 45552 45651: gap of 100 bp
* 45652 46352: contig of 701 bp in length
* 46353 46452: gap of 100 bp
* 46453 47155: contig of 703 bp in length
* 47156 47255: gap of 100 bp
* 47256 47936: contig of 681 bp in length
* 47937 48036: gap of 100 bp
* 48037 48733: contig of 697 bp in length
* 48734 48833: gap of 100 bp
* 48834 49547: contig of 714 bp in length
* 49548 49647: gap of 100 bp
* 49648 50370: contig of 723 bp in length
* 50371 50470: gap of 100 bp
* 50471 51182: contig of 712 bp in length
* 51183 51282: gap of 100 bp

[illegible]

```

Sequencing vector: plasmid; 108752, 97% of reads
Chemistry: Dye-terminator Big Dye, 100% of reads
Consensus quality: 193212 bases at least Q40
Consensus quality: 193979 bases at least Q30
Consensus quality: 194657 bases at least Q20
Insert size: 195602; sum-of-contigs
Insert size: 189734; 3.2% error; agarose-1p
Quality coverage: 8.66x in Q20 bases; sum-of-contigs
Quality coverage: 9.19x in Q20 bases; agarose-1p
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 30237: contig of 30237 bp in length
* 30238 30337: gap of 100 bp
* 30338 34690: contig of 4353 bp in length
* 34691 34790: gap of 100 bp
* 34791 64312: contig of 29522 bp in length
* 64313 64412: gap of 100 bp
* 64413 106093: contig of 41681 bp in length
* 106094 106193: gap of 100 bp
* 106194 127064: contig of 20871 bp in length
* 127065 127164: gap of 100 bp
* 127165 129391: contig of 2227 bp in length
* 129392 129491: gap of 100 bp
* 129492 168470: contig of 38979 bp in length
* 168471 168570: gap of 100 bp
* 168571 170746: contig of 2176 bp in length
* 170747 170846: gap of 100 bp
* 170847 175712: contig of 4866 bp in length
* 175713 175812: gap of 100 bp
* 175813 196502: contig of 20690 bp in length.
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/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-62022"
/clone_lib="RPCT-11.1"
1. .30237
/note="assembly-fragment:03501
fragment_chain:1
clone_end:SP6
vector_side:left"
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/note="assembly-fragment:00992
fragment_chain:1"
34791..64312
/note="assembly-fragment:04019
fragment_chain:1"
64413..106093
/note="assembly-fragment:03224
fragment_chain:2"
106194..127064
/note="assembly-fragment:00432
fragment_chain:2"
127165..129391
/note="assembly-fragment:01059"
129492..168470
/note="assembly-fragment:01373"
168571..170746
/note="assembly-fragment:01732"
170847..175712
/note="assembly-fragment:02462"
175813..196502
/note="assembly-fragment:05361"

```



```

* 25230 26098: contig of 869 bp in length
* 26099 26198: gap of 100 bp
* 26199 27086: contig of 888 bp in length
* 27087 27186: gap of 100 bp
* 27187 28080: contig of 894 bp in length
* 28081 28180: gap of 100 bp
* 28181 29047: contig of 867 bp in length
* 29048 29147: gap of 100 bp
* 29148 30030: contig of 883 bp in length
* 30031 30130: gap of 100 bp
* 30131 30997: contig of 867 bp in length
* 30998 31097: gap of 100 bp
* 31098 31943: contig of 846 bp in length
* 31944 32043: gap of 100 bp
* 32044 32891: contig of 848 bp in length
* 32892 32991: gap of 100 bp
* 32992 33863: contig of 872 bp in length
* 33864 33963: gap of 100 bp
* 33964 34818: contig of 855 bp in length
* 34819 34918: gap of 100 bp
* 34919 35762: contig of 844 bp in length
* 35763 35862: gap of 100 bp
* 35863 36727: contig of 865 bp in length
* 36728 36827: gap of 100 bp
* 36828 37697: contig of 870 bp in length
* 37698 37797: gap of 100 bp
* 37798 38667: contig of 870 bp in length
* 38668 38767: gap of 100 bp
* 38768 39634: contig of 867 bp in length
* 39635 39734: gap of 100 bp
* 39735 40586: contig of 852 bp in length
* 40587 40686: gap of 100 bp
* 40687 41577: contig of 891 bp in length
* 41578 41677: gap of 100 bp
* 41678 42552: contig of 875 bp in length
* 42553 42652: gap of 100 bp
* 42653 43517: contig of 865 bp in length
* 43518 43617: gap of 100 bp
* 43618 44482: contig of 865 bp in length
* 44483 44582: gap of 100 bp
* 44583 45460: contig of 878 bp in length
* 45461 45560: gap of 100 bp
* 45561 46416: contig of 856 bp in length
* 46417 46516: gap of 100 bp
* 46517 47415: contig of 899 bp in length
* 47416 47515: gap of 100 bp
* 47516 48421: contig of 906 bp in length
* 48422 48521: gap of 100 bp
* 48522 49395: contig of 874 bp in length
* 49396 49495: gap of 100 bp
* 49496 50337: contig of 842 bp in length
* 50338 50437: gap of 100 bp
* 50438 51311: contig of 874 bp in length
* 51312 51411: gap of 100 bp
* 51412 52281: contig of 870 bp in length
* 52282 52381: gap of 100 bp
* 52382 53266: contig of 885 bp in length
* 53267 53366: gap of 100 bp
* 53367 54233: contig of 867 bp in length
* 54234 54333: gap of 100 bp
* 54334 55219: contig of 886 bp in length
* 55220 55319: gap of 100 bp
* 55320 56191: contig of 872 bp in length
* 56192 56291: gap of 100 bp
* 56292 57136: contig of 845 bp in length
* 57137 57236: gap of 100 bp
* 57237 58132: contig of 896 bp in length
* 58133 58232: gap of 100 bp
* 58233 59105: contig of 873 bp in length
* 59106 59205: gap of 100 bp
* 59206 60078: contig of 873 bp in length
* 60079 60178: gap of 100 bp
* 60179 61042: contig of 864 bp in length

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* 61043 61142: gap of 100 bp
* 61143 62035: contig of 893 bp in length
* 62036 62135: gap of 100 bp
* 62136 63021: contig of 886 bp in length
* 63022 63121: gap of 100 bp
* 63122 64006: contig of 885 bp in length
* 64007 64106: gap of 100 bp
* 64107 64974: contig of 868 bp in length
* 64975 65074: gap of 100 bp
* 65075 65944: contig of 870 bp in length
* 65945 66044: gap of 100 bp
* 66045 66922: contig of 878 bp in length
* 66923 67022: gap of 100 bp
* 67023 67919: contig of 897 bp in length

Query Match      12.7%  Score 63.4  DB 2:  Length 83440;
Best Local Similarity 45.4%  Pred. No. 4e-05;
Matches 148;  Conservative 0;  Mismatches 178;  Indels 0;  Gaps 0;

QY  125 ttatcgtgtttatcagatgcgattgtgcctcagtgatttgcattatcccaat 184
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  45954 TTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTT 46013

QY  185 aaggttctaccatattttttatcattagtaatgcgtgttcctcgttc 244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  46014 TTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTT 46073

QY  245 tgcgtcttcgtgcgttcctcctctcctcgttcctcgttcgttcgccatgcga 304
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  46074 TTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTT 46133

QY  305 tggcctatacgcgtatatacagagcagtttcaacgcgaagatcctcagttg 364
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  46134 TTTNTTTTNTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTT 46193

QY  365 ctgataccttctacttacttctcgttcttcaaccctacttacttcttctt 424
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  46194 TTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTT 46253

QY  425 tgcacggttttctcctgtactt 450
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  46254 TTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTT 46279

RESULT  15
AC106848/c 8087 bp  DNA  linear  HTG 12-JAN-2002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

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AC106848 Homo sapiens chromosome 8 clone CTD-3149B6 map 8, LOW-PASS SEQUENCE
 AC106848.1 GI:18139484
 HTG: HTGS_PHASE0.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 8087)
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 Homo sapiens chromosome 8, clone CTD-3149B6
 2 (bases 1 to 8087)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
 Brown,A., Camarata,J., Campisano,A., Chang,J., Chazaro,B.,
 Choepel,Y., Colangelo,M., Collins,S., Collinmore,A., Cook,A.,
 Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
 Glade,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
 Jones,C., Kamat,A., Karatas,A., Kellis,G., Lacroque,K.,
 Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
 Maclean,C., Macdonald,P., Major,J., Marguis,N., Matthews,C.,
 McCarthy,M., McEwan,P., McKernan,K., McPheters,R., Meldrum,J.,

